

REMARKS/ARGUMENTS

Applicants thank the Examiner for conducting a telephone interview with the undersigned on December 17, 2004 at which the outstanding office action was discussed. Specifically, the Examiner said that although he found the disclosed utility of forensic analysis of the claimed polymorphisms credible, he was questioning whether the utility was specific and substantial. More particularly, the Examiner questioned whether the claimed polymorphisms could indeed be used to identify different individuals by, for example, the FBI. Applicants pointed out that Table 1 at p. 30 of the specification shows the polymorphic profile in ten individuals at the claimed polymorphic sites (see explanation of Table 1 at p. 8 of the specification). Applicants also pointed out that the polymorphic profile for each individual was different indicating that analysis of the claimed polymorphic sites can be used to distinguish different individuals. The Examiner said that this evidence may be persuasive on further consideration.

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The Examiner then said that the numbering in Table 1 (as originally filed) was displaced by one from the numbering of polymorphic sites in the present claims. This discrepancy was explained in a previous response filed June 18, 2001 and a corrected Table 1 was supplied. In brief, the discrepancy arose because the polymorphic sites in the original Table 1 were numbered in accordance with the first nucleotide being assigned the number zero, rather than 1 as is conventional.

Applicants now turn to the specific comments in the office action.

Claims 1, 3-10 and 15-32 stand rejected under 35 USC 101 for alleged lack of utility. In the previous response, applicants pointed out that the application discloses a credible, substantial and specific utility for the claimed polymorphic sites in forensic analysis. In brief, the utility is credible because it involves standard techniques of molecular biology and statistical analysis. The utility is specific because there are relatively few mitochondrial polymorphisms compared with genomic polymorphisms and mitochondrial polymorphisms offer advantages that they can be detected in small amounts of DNA (due to the presence of large numbers of